

58049-00003 Sequence Listing_ST25
SEQUENCE LISTING

<110> Park, Eun Jeong
Kim, Jang Seong
Jang, Jihoon
Yum, Jungsun
Chung, Soo-il

<120> Novel Detoxified Mutants of Escherichia coli Heat-Labile Enterotoxin

<130> 58049-00003

<140> US 10/088,202

<141> 2002-03-15

<150> PCT/KR99/00555

<151> 1999-09-15

<160> 6

<170> PatentIn version 3.5

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<212> DNA

<213> Artificial sequence

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<223> Primer

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<221> primer_bind

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<213> Escherichia coli

58049-00003 Sequence Listing_ST25

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<222> (1)..(18)

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20 25 30Glu Ile Lys Arg Ser Gly Gly Leu Met Pro Arg Gly His Asn Glu Tyr
35 40 45Phe Asp Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg
50 55 60Gly Thr Gln Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr
65 70 75 80Tyr Leu Ser Leu Arg Ser Ala His Leu Ala Gly Gln Ser Ile Leu Ser
85 90 95Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met
100 105 110Phe Asn Val Asn Asp Val Leu Gly Val Tyr Ser Pro His Pro Tyr Glu
115 120 125Gln Glu Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly
130 135 140Trp Tyr Arg Val Asn Phe Gly Val Ile Asp Glu Arg Leu His Arg Asn
145 150 155 160Arg Glu Tyr Arg Asp Arg Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala
165 170 175Glu Asp Gly Tyr Arg Leu Ala Gly Phe Pro Pro Asp His Gln Ala Trp
180 185 190Arg Glu Glu Pro Trp Ile His His Ala Pro Gln Gly Cys Gly Asn Ser
195 200 205Ser Arg Thr Ile Thr Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu
210 215 220Ser Thr Ile Tyr Leu Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile
Page 2

225 230 58049-00003 Sequence Listing_ST25 235 240

Phe Ser Asp Tyr Gln Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp
245 250 255

Glu Leu Met Asn Lys Val Lys Phe Tyr Val Leu Phe Thr Ala Leu Leu
260 265 270

Ser Ser Leu Cys Ala His Gly Ala Pro Gln Ser Ile Thr Glu Leu Cys
275 280 285

Ser Glu Tyr His Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu
290 295 300

Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr
305 310 315 320

Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His
325 330 335

Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg
340 345 350

Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn
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Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
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tgactctaga	cccccagatg	aaataaaacg	ttccggaggt	cttatgccca	gagggcataa	300
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58049-00003 Sequence Listing_ST25

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Met Lys Asn Ile Thr Phe Ile Phe Phe Ile Leu Leu Ala Ser Pro Leu
 1 5 10 15

Tyr Ala Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp
 20 25 30

Glu Ile Lys Arg Ser Gly Gly Leu Met Pro Arg Gly His Asn Glu Tyr
 35 40 45

Phe Asp Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg
 50 55 60

58049-00003 Sequence Listing_ST25

Gly Thr Gln Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr
65 70 75 80

Ser Leu Ser Leu Arg Ser Ala His Leu Ala Gly Gln Ser Ile Leu Ser
85 90 95

Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met
100 105 110

Phe Asn Val Asn Asp Val Leu Gly Val Tyr Ser Pro His Pro Tyr Gln
115 120 125

Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
130 135 140

Arg Val Asn Phe Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu
145 150 155 160

Tyr Arg Asp Arg Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp
165 170 175

Gly Tyr Arg Leu Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu
180 185 190

Glu Pro Trp Ile His His Ala Pro Gln Gly Cys Gly Asn Ser Ser Arg
195 200 205

Thr Ile Thr Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr
210 215 220

Ile Tyr Leu Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
225 230 235 240

Asp Tyr Gln Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
245 250 255

Met Asn Lys Val Lys Phe Tyr Val Leu Phe Thr Ala Leu Leu Ser Ser
260 265 270

Leu Cys Ala His Gly Ala Pro Gln Ser Ile Thr Glu Leu Cys Ser Glu
275 280 285

Tyr His Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu Ser Tyr
290 295 300

Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr Phe Lys
305 310 315 320

58049-00003 Sequence Listing_ST25

Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
 325 330 335

Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Thr
 340 345 350

Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn Asn Lys
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Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
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58049-00003 Sequence Listing_ST25

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